



O I P E

RAW SEQUENCE LISTING DATE: 02/25/2002
PATENT APPLICATION: US/10/050,726 TIME: 11:22:14

Input Set : N:\CrF3\RULE60\10050726.txt
Output Set: N:\CRF3\02252002\J050726.raw

5 <110> APPLICANT: Pathirana, Marie Sudam
9 <120> TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF68 RECEPTOR
13 <130> FILE REFERENCE: 60795
15 <140> CURRENT APPLICATION NUMBER: 10/050,726
17 <141> CURRENT FILING DATE: 2002-01-16
19 <150> PRIOR APPLICATION NUMBER: 09/466,570
21 <151> PRIOR FILING DATE: 1999-12-17
25 <160> NUMBER OF SEQ ID NOS: 2
29 <170> SOFTWARE: PatentIn Ver. 2.0 - beta
33 <210> SEQ ID NO: 1
35 <211> LENGTH: 1536
37 <212> TYPE: DNA
39 <213> ORGANISM: Homo sapiens
43 <400> SEQUENCE: 1
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47 catggcctta ctgggcagcc a g c a c t c c g g c g c c c c c t c c a c t t g g c g g 120
49 gacttcctcc gcggccacgg c g g c c g t g c t c t c t t c a g c a c c g t g g c g a c c g g c g c t 180
51 ggggaacctg a g c g a c g c a a g c g g a g g c g g c a c a g c t g c c g t c c c c g g t g g c g c t 240
53 tggcgggtcc ggggcagcgc g g g a g g c g g g g c g g g a g g c g g t g a g g c g g c c c t a g g c c g g a 300
55 ggcggcgcg ctgctgtcgc a c g g a g c t g c a g t g g c g c c a g g c g c t c g t c c t c t g c t 360
57 cattttcctg ctgtcttagcc t t g g c a a c t g c g g g t g a t g g g t g a t t g t a g a g c a c c g 420
59 gcagctccgc a c c g t c a c c a a c g c t t c a t c c t g t c g c t g t c c c t a t c g g a t c t g c t a c 480
61 ggcgtgctc t g c c t g c c c g c c g c t t c t g a c c t c t t c a c t c c g c c c g g g g t t c g g c 540
63 gcctgcgcgc g c c g c g g g g c c t g g c g c g g c t t c t g c g c c a g g c c g c t t c t a g c t c 600
65 gtgttcggc a t c g t g t c c a c g t c a g c g t g g c g c t a t c t g t g g a c c t a g c g c 660
67 tatcgtgcgg c c g c c g c g g g a g a a g a t c g g c c c c g c g c t g c a g c t g g c g g g 720
69 cgcctggctg a c g g c c t t g g c t t c t c t g c c t g g g a g g c t g c t g c g g g c g c c c c g g g a 780
71 a c t c g c g g c g g c a g a g c t t c c a c g g c t g c t c t a c c g g a c t t c c c c c g a c c c c g c g a 840
73 gctggcgcg c c t t c a g c g t g g g c t g g t g g c t g a c c t g t c t c t t c t g c t 900
75 catgtgcttc t g c c a c t a c c a c a t c t g c a a g c g g t g c g c t g t c g g a c g t g c g 960
77 g c c g g t g a a c a c t a c g c g c g c t g c t g c g c t t c t t c a g c g a g g t g c g c a c g c c a c c a c 1020
79 cgtcctcata t a g a t c g t c t t c g t c a t c t g c t g c t g t g g g g c c t a c t g c t g c t c t t c t g c t 1080
81 gctggccgccc g c c c g g c a g g c c c a g a c c a t g c a g g c c c c t c g c t c c t c a g c t g g t g g c 1140
83 cgtctggctg a c c t g g c c a a t g g g c c a t c a a c c c t g c t a t c t a c g c c a t c c g c a a t c c 1200
85 caacatttcg a t g c t c c t a g g c g c a a c c g c a a c c g a g g a g g g c t a c c g g a c t a g g a a t g t g g a 1260
87 cgctttccctg c c c a g c c a g g c c c c g g g g t c t g a a g c c a g a a g c c g a t g c t c g a a a 1320
89 ccgctatgcc a a c c g g c t g g q q g c t q c a a c q q a t g t c c t t c c a a c c g g c a g c g 1380
91 a g t g g c a g g g g a c g t g g c c a t g g g c c c g a a a a t c c a g t t g t a c t t t c t g c c g a g a 1440
93 gggaccacca g a g c c g g t g a c g c a g t g a c a a c a c g c t a a a t c c g a a g c t g g g a t a c 1500
95 c a g c c t c t a a g a c g g t g g a a t g g c c a g c t a t g g a a 1536
99 <210> SEQ ID NO: 2
101 <211> LENGTH: 494
103 <212> TYPE: PRT

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105 <213> ORGANISM: Homo sapiens
 109 <400> SEQUENCE: 2
 111 Met Glu Glu Pro Gln Pro Pro Arg Pro Pro Ala Ser Met Ala Leu Leu
 113 1 5 10 15
 117 Gly Ser Gln His Ser Gly Ala Pro Ser Ala Ala Gly Pro Pro Gly Gly
 119 20 25 30
 123 Thr Ser Ser Ala Ala Thr Ala Ala Val Leu Ser Phe Ser Thr Val Ala
 125 35 40 45
 129 Thr Ala Ala Leu Gly Asn Leu Ser Asp Ala Ser Gly Gly Gly Thr Ala
 131 50 55 60
 135 Ala Ala Pro Gly Gly Gly Leu Gly Gly Ser Gly Ala Ala Arg Glu
 137 65 70 75 80
 141 Ala Gly Ala Ala Val Arg Arg Pro Leu Gly Pro Glu Ala Ala Pro Leu
 143 85 90 95
 147 Leu Ser His Gly Ala Ala Val Ala Ala Gln Ala Leu Val Leu Leu Leu
 149 100 105 110
 153 Ile Phe Leu Leu Ser Ser Leu Gly Asn Cys Ala Val Met Gly Val Ile
 155 115 120 125
 159 Val Lys His Arg Gln Leu Arg Thr Val Thr Asn Ala Phe Ile Leu Ser
 161 130 135 140
 165 Leu Ser Leu Ser Asp Leu Leu Thr Ala Leu Leu Cys Leu Pro Ala Ala
 167 145 150 155 160
 171 Phe Leu Asp Leu Phe Thr Pro Pro Gly Gly Ser Ala Pro Ala Ala Ala
 173 165 170 175
 177 Ala Gly Pro Trp Arg Gly Phe Cys Ala Ala Ser Arg Phe Phe Ser Ser
 179 180 185 190
 183 Cys Phe Gly Ile Val Ser Thr Leu Ser Val Ala Leu Ile Ser Leu Asp
 185 195 200 205
 189 Arg Tyr Cys Ala Ile Val Arg Pro Pro Arg Glu Lys Ile Gly Arg Arg
 191 210 215 220
 195 Arg Ala Leu Gln Leu Leu Ala Gly Ala Trp Leu Thr Ala Leu Gly Phe
 197 225 230 235 240
 201 Ser Leu Pro Trp Glu Leu Leu Gly Ala Pro Arg Glu Leu Ala Ala Ala
 203 245 250 255
 207 Gln Ser Phe His Gly Cys Leu Tyr Arg Thr Ser Pro Asp Pro Ala Gln
 209 260 265 270
 213 Leu Gly Ala Ala Phe Ser Val Gly Leu Val Val Ala Cys Tyr Leu Leu
 215 275 280 285
 219 Pro Phe Leu Leu Met Cys Phe Cys His Tyr His Ile Cys Lys Thr Val
 221 290 295 300
 225 Arg Leu Ser Asp Val Arg Val Arg Pro Val Asn Thr Tyr Ala Arg Val
 227 305 310 315 320
 231 Leu Arg Phe Phe Ser Glu Val Arg Thr Ala Thr Thr Val Leu Ile Met
 233 325 330 335
 237 Ile Val Phe Val Ile Cys Cys Trp Gly Pro Tyr Cys Phe Leu Val Leu
 239 340 345 350
 243 Leu Ala Ala Ala Arg Gln Ala Gln Thr Met Gln Ala Pro Ser Leu Leu
 245 355 360 365
 249 Ser Val Val Ala Val Trp Leu Thr Trp Ala Asn Gly Ala Ile Asn Pro

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251	370	375	380
255	Val Ile Tyr Ala Ile Arg Asn Pro Asn Ile Ser Met Leu Leu Gly Arg		
257	385	390	395
261	Asn Arg Glu Glu Gly Tyr Arg Thr Arg Asn Val Asp Ala Phe Leu Pro		400
263		405	410
267	Ser Gln Gly Pro Gly Leu Gln Ala Arg Ser Arg Ser Arg Leu Arg Asn		415
269		420	425
273	Arg Tyr Ala Asn Arg Leu Gly Ala Cys Asn Arg Met Ser Ser Ser Asn		430
275		435	440
279	Phe Ala Ser Gly Val Ala Gly Asp Val Ala Met Trp Ala Arg Lys Asn		445
281		450	455
285	Pro Val Val Leu Phe Cys Arg Glu Gly Pro Pro Glu Pro Val Thr Ala		460
287		465	470
291	Val Thr Lys Gln Pro Lys Ser Glu Ala Gly Asp Thr Ser Leu		475
293		485	490

VERIFICATION SUMMARY

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